



- 1 -

Hq

SEQUENCE LISTING

<110> Lin, Biaoyang

<120> Prostate-Specific Polypeptide PAMP and
Encoding Nucleic Acid Molecules

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<140> US 09/729,653

<141> 2000-12-04

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<221> misc_feature

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Ala	Val	Ala	Cys	Leu	Val	Glu	Thr	Gly	Cys	Ala	Cys	Val	Leu	His	Ser	
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tcg	cgt	agc	ggc	tgc	agc	gtg	gag	atg	aag	cgt	att	ttc	tca	ctg	cta	144
Ser	Arg	Ser	Gly	Ser	Ser	Val	Glu	Met	Lys	Arg	Ile	Phe	Ser	Leu	Leu	
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Glu	Lys	Thr	Trp	Leu	Gly	Ala	Pro	Ile	Gln	Phe	Ala	Trp	Gln	Lys	Thr	
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Ser	Gly	Asn	Tyr	Leu	Ala	Val	Thr	Gly	Ala	Asp	Tyr	Ile	Val	Lys	Ile	
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Cys	Val	Ala	Met	Asp	Trp	Asp	Lys	Asp	Gly	Asp	Val	Leu	Ala	Val	Ile		
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Gln	Phe	Phe	Leu	Met	Lys	Met	Asp	Asp	Arg	Thr	Ser	Ala	Ala	Glu	Ser		
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aac	att	gtc	tgc	tat	aat	tgg	tat	ggg	gat	ggc	cgc	atc	atg	att	ggg	864	
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Phe	Ser	Cys	Gly	His	Phe	Val	Val	Ile	Ser	Thr	His	Thr	Gly	Glu	Leu		

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att gca gta tca cag act ctt aac aaa gtt gct aca tgt gga gat aac			1008
Ile Ala Val Ser Gln Thr Leu Asn Lys Val Ala Thr Cys Gly Asp Asn			
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tgc att aaa atc caa gac ttg gtt gac tta aaa gac atg tat gtt ata			1056
Cys Ile Lys Ile Gln Asp Leu Val Asp Leu Lys Asp Met Tyr Val Ile			
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ctc aac ctg gat gag gaa aat aaa gga ttg ggt acc ttg tcc tgg act			1104
Leu Asn Leu Asp Glu Glu Asn Lys Gly Leu Gly Thr Leu Ser Trp Thr			
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Asp Asp Gly Gln Leu Leu Ala Leu Ser Thr Gln Arg Gly Ser Leu His			
	370	375	380
gtt ttc ctg acc aag ctt ccc ata ctt ggg gat gcc tgc agc aca agg			1200
Val Phe Leu Thr Lys Leu Pro Ile Leu Gly Asp Ala Cys Ser Thr Arg			
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Ile Ala Tyr Leu Thr Ser Leu Leu Glu Val Thr Val Ala Asn Pro Val			
	405	410	415
gaa gga gag cta cca atc aca gtt tct gtt gat gtg gaa ccc aac ttt			1296
Glu Gly Glu Leu Pro Ile Thr Val Ser Val Asp Val Glu Pro Asn Phe			
	420	425	430
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Val Ala Val Gly Leu Tyr His Leu Ala Val Gly Met Asn Asn Arg Ala			
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Trp Phe Tyr Val Leu Gly Glu Asn Ala Val Lys Lys Leu Lys Asp Met			
	450	455	460
gag tat ctg gga aca gta gcc agt att tgc ctt cat tct gac tat gct			1440
Glu Tyr Leu Gly Thr Val Ala Ser Ile Cys Leu His Ser Asp Tyr Ala			
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gct gca ctt ttt gaa ggc aaa gtc cag tta cat ttg ata gaa agc gaa			1488
Ala Ala Leu Phe Glu Gly Lys Val Gln Leu His Leu Ile Glu Ser Glu			
	485	490	495
atc ttg gat gct caa gaa gaa cgt gag act cgg ctt ttc cca gca gtg			1536
Ile Leu Asp Ala Gln Glu Glu Arg Glu Thr Arg Leu Phe Pro Ala Val			
	500	505	510

gat gat aag tgc cgt atc tta tgc cat gcc tta act agt gat ttc ctc	1584
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515 520 525	
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Ile Tyr Gly Thr Asp Thr Gly Val Val Gln Tyr Phe Tyr Ile Glu Asp	
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Trp Gln Phe Val Asn Asp Tyr Arg His Pro Val Ser Val Lys Lys Ile	
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Phe Pro Asp Pro Asn Gly Thr Arg Leu Val Phe Ile Asp Glu Lys Ser	
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Asp Lys Gly Val Phe Ile Ala Tyr Asp Asp Asp Lys Val Tyr Thr Tyr	
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Val Phe His Lys Asp Thr Ile Gln Gly Ala Lys Val Ile Leu Ala Gly	
625 630 635 640	
agc acc aaa gtt cct ttt gct cat aaa cct ttg ctg cta tat aat gga	1968
Ser Thr Lys Val Pro Phe Ala His Lys Pro Leu Leu Leu Tyr Asn Gly	
645 650 655	
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Glu Leu Thr Cys Gln Thr Gln Ser Gly Lys Val Asn Asn Ile Tyr Leu	
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agc acc cat ggc ttt ctc agc aac tta aaa gat asg ggg cct gac gaa	2064
Ser Thr His Gly Phe Leu Ser Asn Leu Lys Asp Xaa Gly Pro Asp Glu	
675 680 685	
ctg aga cca atg ctg gca cac aat tta atg cta aag agg ttt tct gat	2112
Leu Arg Pro Met Leu Ala His Asn Leu Met Leu Lys Arg Phe Ser Asp	
690 695 700	
gct tgg gaa atg tgc agg att ctg aat gat gag gct gcc tgg aat gag	2160
Ala Trp Glu Met Cys Arg Ile Leu Asn Asp Glu Ala Ala Trp Asn Glu	
705 710 715 720	

ttg gcc aga gct tgt' cta cat cac atg gaa gtg gag ttt gca atc cgt	2208
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Val Tyr Arg Arg Ile Gly Asn Val Gly Ile Val Met Ser Leu Glu Gln	
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ata aag gga ata gag gac tac aat ctt ttg gca gga cac ctt gcc atg	2304
Ile Lys Gly Ile Glu Asp Tyr Asn Leu Leu Ala Gly His Leu Ala Met	
755 760 765	
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Phe Thr Asn Asp Tyr Asn Leu Ala Gln Asp Leu Tyr Leu Ala Ser Ser	
770 775 780	
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Cys Pro Ile Ala Ala Leu Glu Met Arg Arg Asp Leu Gln His Trp Asp	
785 790 795 800	
agt gct cta caa ctg gca aag cat ttg gcc cca gac cag ata cct ttt	2448
Ser Ala Leu Gln Leu Ala Lys His Leu Ala Pro Asp Gln Ile Pro Phe	
805 810 815	
ata tca aaa gaa tat gct att cag ctt gaa ttc gcg ggt gat tat gta	2496
Ile Ser Lys Glu Tyr Ala Ile Gln Leu Glu Phe Ala Gly Asp Tyr Val	
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aat gct ttg gct cat tat gag aaa gga ata aca ggt gat aat aag gaa	2544
Asn Ala Leu Ala His Tyr Glu Lys Gly Ile Thr Gly Asp Asn Lys Glu	
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cat gat gaa gct tgt ctg gct gga gtg gcc cag atg tcc ata aga atg	2592
His Asp Glu Ala Cys Leu Ala Gly Val Ala Gln Met Ser Ile Arg Met	
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gga gac ata cgt cga ggg gtt aac caa gcc ctc aag cat ccc agc agg	2640
Gly Asp Ile Arg Arg Gly Val Asn Gln Ala Leu Lys His Pro Ser Arg	
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gtc ctt aaa aga gac tgt gga gcc ata ttg gag aat atg aag caa ttt	2688
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Ser Glu Ala Ala Gln Leu Tyr Glu Lys Gly Leu Tyr Tyr Asp Lys Ala	
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gca tct gtt tac atc cgc tct aag aat tgg gca aaa gtt ggt gat ctt	2784
Ala Ser Val Tyr Ile Arg Ser Lys Asn Trp Ala Lys Val Gly Asp Leu	
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ctg ccc cac gtt tct tct cct aag atc cat ttg cag tat gcc aaa gcc	2832

Leu	Pro	His	Val	Ser	Ser	Pro	Lys	Ile	His	Leu	Gln	Tyr	Ala	Lys	Ala		
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Lys	Glu	Ala	Asp	Gly	Arg	Tyr	Lys	Glu	Ala	Val	Val	Ala	Tyr	Glu	Asn		
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Ala	Lys	Gln	Trp	Gln	Ser	Val	Ile	Arg	Ile	Tyr	Leu	Asp	His	Leu	Asn		
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aat	cct	gaa	aaa	gct	gtc	aat	att	gtt	aga	gag	acc	cag	tct	ctg	gat	2976	
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tct	gcc	atc	cag	ttt	ctt	gtc	atg	tcc	aaa	tgc	aac	aat	gaa	gct	ttc	3072	
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Thr	Leu	Ala	Gln	Gln	His	Asn	Lys	Met	Glu	Ile	Tyr	Ala	Asp	Ile	Ile		
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Gly	Ser	Glu	Asp	Thr	Thr	Asn	Glu	Asp	Tyr	Gln	Ser	Ile	Ala	Leu	Tyr		
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Phe	Glu	Gly	Glu	Lys	Arg	Tyr	Leu	Gln	Ala	Gly	Lys	Phe	Phe	Leu	Leu		
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Lys Ile His Val Lys Asn Gly Asp His Met Lys Gly Ala Arg Met Leu			
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Ser Ala Phe Ser Phe Ala Ala Met Leu Met Arg Pro Glu Tyr Arg Ser			
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Lys Ile Asp Ala Lys Tyr Lys Lys Lys Ile Glu Gly Met Val Arg Arg			
1265	1270	1275	1280
ccc gat ata tct gag ata gaa gag gcc acg act cca tgt cca ttc tgc			3888
Pro Asp Ile Ser Glu Ile Glu Glu Ala Thr Thr Pro Cys Pro Phe Cys			
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aaa ttt ctt ctc cca gag tgt gaa ctc ctc tgt cct gga tgt aaa aac			3936
Lys Phe Leu Leu Pro Glu Cys Glu Leu Leu Cys Pro Gly Cys Lys Asn			
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agt atc cca tat tgc att gca aca ggt cga cac atg ttg aaa gat gac			3984
Ser Ile Pro Tyr Cys Ile Ala Thr Gly Arg His Met Leu Lys Asp Asp			
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Trp Thr Val Cys Pro His Cys Asp Phe Pro Ala Leu Tyr Ser Glu Leu			
1330	1335	1340	
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Lys Ile Met Leu Asn Thr Glu Ser Thr Cys Pro Met Cys Ser Glu Arg			
1345	1350	1355	1360

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 1365 1370 1375

cga acg gag gag gaa ctg tgattggcac gtgcagatac aatgctcctg 4176
 Arg Thr Glu Glu Glu Leu
 1380

agaagacagc attttccaca ggaggctgtt tcctcccctg gtggatttaa gagacgggcc 4236
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<210> 2
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 <213> Homo sapien

<220>
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 <222> (1)...(1382)
 <223> Xaa = Any Amino Acid

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 35 40 45
 Glu Lys Thr Trp Leu Gly Ala Pro Ile Gln Phe Ala Trp Gln Lys Thr
 50 55 60
 Ser Gly Asn Tyr Leu Ala Val Thr Gly Ala Asp Tyr Ile Val Lys Ile
 65 70 75 80
 Phe Asp Arg His Gly Gln Lys Arg Ser Glu Ile Asn Leu Pro Gly Asn
 85 90 95
 Cys Val Ala Met Asp Trp Asp Lys Asp Gly Asp Val Leu Ala Val Ile
 100 105 110
 Ala Glu Lys Ser Ser Cys Ile Tyr Leu Trp Asp Ala Asn Thr Asn Lys
 115 120 125
 Thr Ser Gln Leu Asp Asn Gly Met Arg Asp Gln Met Ser Phe Leu Leu
 130 135 140
 Trp Ser Lys Val Gly Ser Phe Leu Ala Val Gly Thr Val Lys Gly Asn
 145 150 155 160
 Leu Xaa Ile Tyr Asn His Gln Thr Ser Arg Lys Ile Pro Val Leu Gly
 165 170 175
 Lys His Thr Lys Arg Ile Thr Cys Gly Cys Trp Asn Ala Glu Asn Leu
 180 185 190
 Xaa Ala Leu Gly Gly Glu Asp Lys Met Ile Thr Val Ser Asn Gln Glu
 195 200 205

Gly	Asp	Thr	Ile	Arg	Gln	Thr	Gln	Val	Arg	Ser	Glu	Pro	Xaa	Asn	Met
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225					230					235					240
Met	Ile	Ser	Val	Val	Leu	Gly	Lys	Lys	Thr	Leu	Phe	Phe	Leu	Asn	Leu
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Asn	Glu	Pro	Asp	Asn	Pro	Ala	Asp	Leu	Glu	Phe	Gln	Gln	Asp	Phe	Gly
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Glu	Gly	Glu	Leu	Pro	Ile	Thr	Val	Ser	Val	Asp	Val	Glu	Pro	Asn	Phe
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Ala	Ala	Leu	Phe	Glu	Gly	Lys	Val	Gln	Leu	His	Leu	Ile	Glu	Ser	Glu
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